

```

1 AATGGATTGG ACTCCGGTGG GGAAAGCGGG TGTCTAGAAG TGGTGCTAAT
51 GGAAGAGAGAA TTCTGGTTTC AAAAGAGGAT GCTCTGCCAC AAAGAGCGGC
101 TCGCGCGCTG GCCTGGGCTC TAGCCGAGGA GAGATCCCGG GAGAACTCCA
151 GAGCTCCGGG GGAGCGCTCC TCGGAAGACC GGGGCCAACA TGCCTGTGCG
201 CAGGGGGCAT GTGGCACCAC AAAATACATT TCTGGGGACC ATCATTCGGA
251 AATTGAAGG GCAAAATAAA AAATTTATCA TTGCAAATGC CAGAGTGCAG
301 AACTGTGCCA TCATTTATTG CAACGATGGG TTCTGTGAGA TGA CTGTTT
351 CTCCAGGCCA GATGTCATGC AAAAGCCATG CACCTGCGAC TTTCTCCATG
401 GACCCGAGAC CAAGAGGCAT GATATTGCCC AAATTGCCCC GGCATTGCTG
451 GGGTCAGAAG AGAGGAAAGT GGAGGTCACC TACTATCACA AAAATGGGTC
501 CACTTTTATT TGTAACACTC ACATAATTCC AGTGAAAAAC CAAGAGGGCG
551 TGGCTATGAT GTTCATCATT AATTTTGAAT ATGTGACGGA TAATGAAAAAC
601 GCTGCCACCC CAGAGAGGGT AAACCCAATA TTACCAATCA AAAGTGTAAA
651 CCGGAAATTT TTTGGGTTC AATTCCCTGG TCTGAGACTT CTCACTTACA
701 GAAAGCAGTC CTTACCACAA GAAGACCCCG ATGTGGTGGT CATCGATTCA
751 TCTAAACACA GTGATGATTC AGTAGCCATG AAGCATTTTA AGTCTCCTAC
801 AAAAGAAAGC TGCAGCCCCCT CTGAAGCAGA TGACACAAAA GCTTTGATAC
851 AGCCCAGCAA ATGTTCTCCC TTGGTGAATA TATCCGGACC TCTTGACCAT
901 TCCTCTCCCA AAAGGCAATG GGACCGACTC TACCCTGACA TGCTGCAGTC
951 AAGTTCCOCAG CTGTCCCAT TCCAGATCAAG GGAAAGCTTA TGTA GTATAC
1001 GGAGAGCATC TTCGGTCCAT GATATAGAAG GATTGCGCGT CCACCCCAAG
1051 AACATATTTA GAGACCGACA TGCCAGCGAA GACAATGGTC GCAATGTCAA
1101 AGTTTACAGT TCCTGGATGG CAGGGGGGCC TTTTAATCAT ATCAAGTCAA
1151 GCCTCCTGGG ATCCACATCA GATTCAAACC TCAACAAATA CAGCACCATT
1201 AACAGATTTC CACAGCTCAC TCTGAATTTT TCAGAGGTCA AAAGTGAGAA
1251 AAAGAATTCA TCACCTCCTT CTTCAGATAA AACCATTATT GCACCCAAGG
1301 TTAAAGATCG AACACACAAT GTGACTGAGA AAGTGACCCA GGTTCCTCTCT
1351 TTAGGAGCAG ATGTCCTACC TGAATACAAA CTGCAGACAC CACGCATCAA
1401 CAAGTTTACG ATATTGCACT ACAGCCCTTT CAAGGCAGTC TGGGACTGGC
1451 TTATCCTGCT GTTGGTCATA TACACTGCTA TATTTACTCC CTACTCTGCA
1501 GCCTTCTCTC TCAATGACAG AGAAGAACAG AAAAGACGAG AATGTGGCTA
1551 TTCTTGTAGC CCTTTGAATG TGGTAGACTT GATTGTGGAT ATTATGTTTA
1601 TCATAGATAT TTTAATAAAC TTCAGAACAA CATATGTAAA TCAGAATGAA
1651 GAAGTGGTAA GTGATCCCGC CAAAATAGCA ATACACTACT TCAAAGGCTG
1701 GTTCCTGATT GACATGGTTG CAGCAATTCC TTTTGA CTGATT TTTG
1751 GATCAGGTTT TGATGAGGTA AGAACTGCTT AAGATTCTTA TTTTCTGAAA
1801 GATTGCAATT ATAAAAGTGA ATCTATTTTA ACTGCAAAAA GAAGAGTTGC
1851 TTTGCAAGCT TCTTGTATCT CACTGATAAA ATTCATTTTC AATTGGGGAT
1901 ACTACAGAAT GAAATGAAAC CATTTTGCCA TTGCAAATCA AATTCTTTCT
1951 CTTTTTGCTA AGAGATGCAA AAGATTCTCC ATTCTTTACC CACCAAATTA
2001 AACTTGGAAG CAAGTGGTCC ATAGCACACA GCACATTTCC AGGATTTAAA
2051 ATCTCTACTT ATTAAC TTCA CGGGTGTAAT ACTCTCAAT ATTAAGTATG
2101 TCTCTGTTTT TCTTAACTCA TTGTTAAGGG TTTGAGACAG CAGAGATTTG
2151 GTTTTTTTGT TCAAATTATT GTGAAGAGGG CCCCTTTTCC GAAAT (SEQ ID NO:1)

```

**FEATURES:**

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5'UTR:      1-189
Start Codon: 190
Stop Codon:  1780
3'UTR:      1783

```

# **HOMOLOGOUS PROTEINS:**

## Top 10 BLAST Hits:

	Score	E
CRA 113000007753533 /altid=gi 4104136 /def=gb AAD01946.1  (AF03...	1058	0.0
CRA 36000087530063 /altid=gi 11121258 /def=emb CAC14797.1  (AJ2...	1041	0.0
CRA 18000005124020 /altid=gi 2745727 /def=gb AAB94741.1  (AF016...	1039	0.0
CRA 18000005107889 /altid=gi 7305203 /def=ref NP_038597.1  pota...	592	e-168
CRA 18000005107891 /altid=gi 2582015 /def=gb AAC53420.1  (AF012...	591	e-168
CRA 18000005084931 /altid=gi 2190505 /def=emb CAB09536.1  (Z961...	589	e-167
CRA 18000004922641 /altid=gi 4557729 /def=ref NP_000229.1  pota...	580	e-164
CRA 108000024648805 /altid=gi 12733048 /def=ref XP_004743.2  po...	580	e-164
CRA 164000136746223 /altid=gi 11933152 /def=dbj BAB19682.1  (AB...	580	e-164
CRA 1000737074349 /altid=gi 6687230 /def=emb CAB64868.1  (AJ243...	570	e-161

## BLAST dbEST hit:

gi 2229460 /dataset=dbest /taxon=9606 ...	434	e-119
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# **EXPRESSION INFORMATION FOR MODULATORY USE:**

library source:

From BLAST dbEST hit:

gi|2229460 testis

From tissue screening panels:

whole\_brain

```

1 MPVRRGHVAP QNTFLGTIIR KFEGQNKKEI IANARVQNC A IYCNDGFCE
51 MTGFSRPDVM QKPCTCDFLH GPETKRHDIA QIAQALLGSE ERKVEVTTYH
101 KNGSTFICNT HIIPVKNQEG VAMMFLINFE YVTDNENAAT PERVNPILPI
151 KTVNRKFFGF KFPGLRLTY RKQSLPQEDP DVVVIDSSKH SDDSVAMKHF
201 KSPTKESCSF SEADDTKALI QPSKCSPLVN ISGPLDHSSP KRQWDRLYPD
251 MLQSSSQLSH SRSRESLCSI RRASSVHDIE GFGVHPKNIF RDRHASEDNG
301 RNVKVSRSWM AGGPFNHIKS SLLGSTSDSN LNKYSTINKI PQLTLNFSEV
351 KTEKKNSSPP SSDKTIIAPK VKDRTHNVTE KVTQVLSLGA DVLPEYKLQT
401 PRINKFTILH YSPFKAVWDW LILLLLVIYA IFTPYSA AFL LNDREEQKRR
451 ECGYSCSPLN VVDLIVDIMF IIDILINERT TYVNQNEEVV SDPAKIAIHY
501 FKGWFLIDMV AAIPFDLLIF GSGSDEVRTA (SEQ ID NO:2)

```

#### FEATURES:

##### Functional domains and key regions:

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION

N-glycosylation site

Number of matches: 4

```

1 102-105 NGST
2 230-233 NISG
3 346-349 NFSE
4 377-380 NVTE

```

[2] PDOC00004 PS00004 CAMP\_PHOSPHO\_SITE

CAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 3

```

1 171-174 RKQS
2 271-274 RRAS
3 354-357 KKNS

```

[3] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE

Protein kinase C phosphorylation site

Number of matches: 9

```

1 74-76 TKR
2 169-171 TYR
3 187-189 SSK
4 239-241 SPK
5 269-271 SIR
6 352-354 TEK
7 379-381 TEK
8 362-364 SDK
9 352-354 TEK

```

[4] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE

Casein kinase II phosphorylation site

Number of matches: 7

```

1 55-58 SRPD
2 133-136 TDNE
3 209-212 SPSE
4 211-214 SEAD
5 275-278 SVHD
6 325-328 STSD
7 522-525 SGSD

```

[5] PDOC00007 PS00007 TYR\_PHOSPHO\_SITE  
Tyrosine kinase phosphorylation site

Number of matches: 3

1 92-99 RKVEVTTY  
2 241-248 KRQWDRLY  
3 448-454 KRRECGY

[6] PDOC00008 PS00008 MYRISTYL  
N-myristoylation site

312-317 GGPFNH

**Membrane spanning structure and domains:**

Helix	Begin	End	Score	Certainty
1	420	440	1.885	Certain
2	504	524	1.071	Certain

# **BLAST Alignment to Top Hit:**

```
>CRA|113000007753533 /altid=gi|4104136 /def=gb|AAD01946.1|
(AF032897) potassium channel subunit [Homo sapiens]
/org=Homo sapiens /taxon=9606 /dataset=nraa /length=1196
Length = 1196
```

Score = 1058 bits (2705), Expect = 0.0  
Identities = 518/529 (97%), Positives = 519/529 (97%), Gaps = 8/529 (1%)

```
Query: 1  MPVRRGHVAPQNTFLGTIIRKFEGQNKKFIIANARVQNCIIYCNDGFCEMTGFSRPDVM 60
          MPVRRGHVAPQNTFLGTIIRKFEGQNKKFIIANARVQNCIIYCNDGFCEMTGFSRPDVM
Sbjct: 1  MPVRRGHVAPQNTFLGTIIRKFEGQNKKFIIANARVQNCIIYCNDGFCEMTGFSRPDVM 60

Query: 61  QKPCTCDFLHGPETKRHDIAQIAQALLGSEERKVEVTTYHKNKGSTFICNTHIIPVKNQEG 120
          QKPCTCDFLHGPETKRHDIAQIAQALLGSEERKVEVTTYHKNKGSTFICNTHIIPVKNQEG
Sbjct: 61  QKPCTCDFLHGPETKRHDIAQIAQALLGSEERKVEVTTYHKNKGSTFICNTHIIPVKNQEG 120

Query: 121 VAMMFIINFEYVTDNENAATPERVNPILPIKTVNRKFFGFKFGLRLLTYRKQSLPQEDP 180
          VAMMFIINFEYVTDNENAATPERVNPILPIKTVNRKFFGFKFGLR+LTYRKQSLPQEDP
Sbjct: 121 VAMMFIINFEYVTDNENAATPERVNPILPIKTVNRKFFGFKFGLRVLTYRKQSLPQEDP 180

Query: 181 DVVVIDSSKHSDDSVAMKHFKSPTEKSCSPSEADDTKALIQPSKCSPLVNISGPLDHSSP 240
          DVVVIDSSKHSDDSVAMKHFKSPTEKSCSPSEADDTKALIQPSKCSPLVNISGPLDHSSP
Sbjct: 181 DVVVIDSSKHSDDSVAMKHFKSPTEKSCSPSEADDTKALIQPSKCSPLVNISGPLDHSSP 240

Query: 241 KRQWDRLYPDMLQSSSQLSHSRRESLCSIRRASSVHDIEGFGVHPKNI FRDRHASEDNG 300
          KRQWDRLYPDMLQSSSQLSHSRRESLCSIRRASSVHDIEGFGVHPKNI FRDRHASEDNG
Sbjct: 241 KRQWDRLYPDMLQSSSQLSHSRRESLCSIRRASSVHDIEGFGVHPKNI FRDRHASEDNG 300

Query: 301 RNVKVSRSWMAGGPFNHKSSLLGSTSDSNLNKYSTINKIPQLTLNFSEVKTEKKNSSPP 360
          RNVK          GPFNHKSSLLGSTSDSNLNKYSTINKIPQLTLNFSEVKTEKKNSSPP
Sbjct: 301 RNVK-----GPFNHKSSLLGSTSDSNLNKYSTINKIPQLTLNFSEVKTEKKNSSPP 352

Query: 361 SSDKTIIAPKVKDRTHNVTEKVTQVLSLGADVLPEYKLQTPRINKFTILHYSFPKAVWDW 420
          SSDKTIIAPKVKDRTHNVTEKVTQVLSLGADVLPEYKLQTPRINKFTILHYSFPKAVWDW
Sbjct: 353 SSDKTIIAPKVKDRTHNVTEKVTQVLSLGADVLPEYKLQTPRINKFTILHYSFPKAVWDW 412

Query: 421 LILLLVIIYTAIFTTPYSAAFLNDREEQKRRECGYSCSPLNVVDLIVDIMFIIDILINFRT 480
          LILLLVIIYTAIFTTPYSAAFLNDREEQKRRECGYSCSPLNVVDLIVDIMFIIDILINFRT
Sbjct: 413 LILLLVIIYTAIFTTPYSAAFLNDREEQKRRECGYSCSPLNVVDLIVDIMFIIDILINFRT 472

Query: 481 TYVNQNEEVVSDPAKIAIH YFKGWFLIDMVAAIPFDLLIFGSGSDEVRT 529
          TYVNQNEEVVSDPAKIAIH YFKGWFLIDMVAAIPFDLLIFGSGSDE T
Sbjct: 473 TYVNQNEEVVSDPAKIAIH YFKGWFLIDMVAAIPFDLLIFGSGSDETTT 521 (SEQ ID NO:4)
```

## **Hmmer search results (Pfam):**

Model	Description	Score	E-value	N
PF00914	Transmembrane region cyclic Nucleotide Gated	34.2	1.4e-08	1
CE00367	E00367 brain_cyclic_nucleotide_gated_channel	30.3	5.1e-08	1
PF00785	PAC motif	16.2	0.006	1
PF00989	PAS domain	6.4	3.7	1

## **Parsed for domains:**

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00989	1/1	41	60 ..	26	45 ..	6.4	3.7
PF00785	1/1	93	120 ..	1	28 [.	16.2	0.006
CE00367	1/1	467	516 ..	92	142 ..	30.3	5.1e-08
PF00914	1/1	500	526 ..	1	28 [.	34.2	1.4e-08